



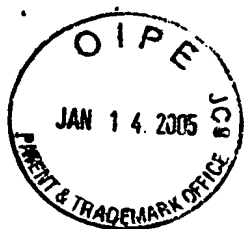
7/13

FIGURE 6A

SEQ ID NO:8 (nucleic acid sequence)

SEQ ID NO:7 (amino acid sequence)

-792	CTTAAATACCAATAGGAAAATTATCAATAAAGCTTTTCGGATTTTCATTACGTTATATC	-733
-732	GCAAAAAAATAGTCGAGCTTTCTGAACCGTTTCGTTAATAAAAAAATAGTTTTTTCAGATT	-673
-672	TCTATGTGAGGCAGTCACGATAGAATTCCATCGAACTCGTCAGCGCCAAATGTGAATGOG	-613
-612	GCTTTCAAAGCTTTGTGCAATTTGGGATGGGAATCCATGAATCGAAGATGTCAAATGG	-553
-552	GGGATCACAAAAGTACACTCAGGAGGAAAATCAAACCTTCTCGTACCTTTAACACATAC	-493
-492	GGAAATGATCGATCGATTTTGAGAAGATTCCTCAATGATTTTCGTATATATAGGTATCTG	-433
-432	AGGTATTTATGGACCGATTCTGTAATAACATCATATACATCGCGCTTTGTCCCTGTCCAG	-373
-372	AGATTTTCGATGAAAAAAGCGAATTTTATTCTAATATTTGAAGCATGCCAAACATGGGGCA	-313
-312	GTGATTTGTGTGAGGGTAAATATCATGAATTGCACCCATCAAATGCAGCAAGATATTG	-253
-252	ACCAATCCTATAATAGAAAACAGACTTACCACAAATAGATTGTGATGACGATATTATGAA	-193
-192	TCTCCAGATGAAAGGCTCGAAAGCTATGAAGCCTCTTGAAACTTTTCATGGTGAGATAAT	-133
-132	ATTTTCGAAATTTCCACGAACCTTCTAAAACGCAATTATTGAATATAAAGGAAAAATAATA	-73
-72	TTTCCATATAGCAAGCAAATCAAGCTGCACTCCTCATCTTAAACTAATAAATCTTACC	-13
-12	CATTTGATACCAATGGTCAAAGGTAATGTTATAGTGGTTTCAAATAGAATCCCGACT	48
1	MetValLysGlyAsnValIleValValSerAsnArgIleProValThr	16
49	ATTAAGAAGACTGAAGATGATGAAAATGGAAAATCAAGATACGACTATACAATGTCATCA	108
17	IleLysLysThrGluAspAspGluAsnGlyLysSerArgTyrAspTyrThrMetSerSer	36
109	GGCGGATTAGTGACGGCATTACAAGGGCTCAAAAATCCATTTTCGATGGTTTGGATGGCCT	168
37	GlyGlyLeuValThrAlaLeuGlnGlyLeuLysAsnProPheArgTrpPheGlyTrpPro	56
169	GGGATGTCTGTTGATAGCGAACAGGGACGACAAACTGTGAGCGGGATTGGAAGGAAAAG	228
57	GlyMetSerValAspSerGluGlnGlyArgGlnThrValGluArgAspLeuLysGluLys	76
229	TTCAATTGTTATCCGATATGGTTAAGTGACGAAATGCAGACTTACATTATAACGGCTTT	288
77	PheAsnCysTyrProIleTrpLeuSerAspGluIleAlaAspLeuHisTyrAsnGlyPhe	96
289	AGCAATTCTATACTTTGGCCATTGTTCCACTATCACCCAGGGAGATGAATTTTGATGAA	348
97	SerAsnSerIleLeuTrpProLeuPheHisTyrHisProGlyGluMetAsnPheAspGlu	116
349	ATTGCTTGGGCCGCTTATTTGGAAGCAAATAAACTGTTTTGCCAAACGATCTTAAAGGAG	408
117	IleAlaTrpAlaAlaTyrLeuGluAlaAsnLysLeuPheCysGlnThrIleLeuLysGlu	136
409	ATAAAGACGGGGACGTTATCTGGGTACATGATTATCATCTCATGTTGTTGCCTTCACTG	468
137	IleLysAspGlyAspValIleTrpValHisAspTyrHisLeuMetLeuLeuProSerLeu	156
469	CTAAGAGACCAACTTAATAGTAAGGGGCTACCGAATGTCAAATTTGGCTTTTTCTTCAT	528
157	LeuArgAspGlnLeuAsnSerLysGlyLeuProAsnValLysIleGlyPhePheLeuHis	176
529	ACTCCTTTTCCTTCAAGCGAAATATACAGGATACTTCTGTAAAGGAAAGAAATTCTCGAA	588
177	ThrProPheProSerSerGluIleTyrArgIleLeuProValArgLysGluIleLeuGlu	196
589	GGAGTGCTTAGTTGTGATTTGATAGGTTTCCACACCTATGATTATGTCCGTCACTTTCTT	648
197	GlyValLeuSerCysAspLeuIleGlyPheHisThrTyrAspTyrValArgHisPheLeu	216
649	AGTTTCGGTTGAAAGAATATTGAAATTGCGAACGAGCCCAAGGTGTTGTCTATAATGAT	708
217	SerSerValGluArgIleLeuLysLeuArgThrSerProGlnGlyValValTyrAsnAsp	236



8/13

FIGURE 6B

709	AGACAGGTGACTGTAAAGTGCTTATCCGATTGGCATTGACGTTGACAAATTCTTGAATGGT	768
237	ArgGlnValThrValSerAlaTyrProIleGlyIleAspValAspLysPheLeuAsnGly	256
769	CTTAAGACTGATGAGGTCAAAGCAGGATAAAACAGCTGGAAACCAGATTTGGTAAAGAT	828
257	LeuLysThrAspGluValLysSerArgIleLysGlnLeuGluThrArgPheGlyLysAsp	276
829	TGTAAACTTATTATTGGGGTGGACAGGCTGGATTACATCAAAGGTGTACCTCAAAACTC	888
277	CysLysLeuIleIleGlyValAspArgLeuAspTyrIleLysGlyValProGlnLysLeu	296
889	CACGCGTTTGAAATTTTCTTGGAGAGACACCCTGAGTGGATTGGAAAAGTTGTTTTGATA	948
297	HisAlaPheGluIlePheLeuGluArgHisProGluTrpIleGlyLysValValLeuIle	316
949	CAGGTGGCTGTCCCTCACGAGGGGACGTTGAAGAATATCAATCTTTGAGGGCAGCTGTA	1008
317	GlnValAlaValProSerArgGlyAspValGluGluTyrGlnSerLeuArgAlaAlaVal	336
1009	AATGAGCTAGTGGGAAGAATCAATGGTAGATTTGGTACCGTCGAATTTGTTTCCTATCCAT	1068
337	AsnGluLeuValGlyArgIleAsnGlyArgPheGlyThrValGluPheValProIleHis	356
1069	TTCCTTCATAAAAGCGTGAACCTCCAAGAGCTGATATCTGTCTACGCTGCTAGTGATGTT	1128
357	PheLeuHisLysSerValAsnPheGlnGluLeuIleSerValTyrAlaAlaSerAspVal	376
1129	TGIGTAGTGTTCATCGACACGGGACGGAATGAATTTGGTCAGTTATGAATACATTGCTTGT	1188
377	CysValValSerSerThrArgAspGlyMetAsnLeuValSerTyrGluTyrIleAlaCys	396
1189	CAACAAGATCGAAAGGGATCTCTAGTACTAAGTGAATTTGCGGGAGCTGCTCAGTCATTA	1248
397	GlnGlnAspArgLysGlySerLeuValLeuSerGluPheAlaGlyAlaAlaGlnSerLeu	416
1249	AATGGCGCTCTCGTAGTGAATCCATGGAATACAGAAGAACTCAGTGAAGCTATTTACGAA	1308
417	AsnGlyAlaLeuValValAsnProTrpAsnThrGluGluLeuSerGluAlaIleTyrGlu	436
1309	GGCTTGATCATGAGTGAAGAGAAAAGGAGGGGCAATTTTCAGAAGATGTTCAAGTACATT	1368
437	GlyLeuIleMetSerGluGluLysArgArgGlyAsnPheGlnLysMetPheLysTyrIle	456
1369	GAGAAATATACTGCAAGTTATTGGGGAGAGAACTTTGTGAAAGAATTGACGAGAGTGTGA	1428
457	GluLysTyrThrAlaSerTyrTrpGlyGluAsnPheValLysGluLeuThrArgVal	476
1429	TTACTGTGGTTTGCAGGTTAATTTGAAATGTTCACTTGTACTTGAAGAATTTTATATTAT	1488
1489	ATACATGTTATACATCAATAGGATAAAAATTAAGTAGACAAAGTTATCATTTTGTGGGC	1548
1549	TGTAAAAATTGAACGATAACAATATATTTGACAAAATTAATTTGATCTAATTGAGCTGGA	1608
1609	GGGCGTAATATATTTGGTTTCCTGAATCATCTTGTAGATCACAATATGGGGCAGCTTCTT	1668
1669	TCGCAGCCGATCACAGAGAAACACATCACACTTGTCCAACATGATCACATATCGCATTCA	1728
1729	ATCGGGGAAATGCAAGGATACAGGTTGACCATGGAAGACGCGTTCTGTGATTGTAACGAA	1788
1789	AGAATATTCTGTGACGGAAGAGGGACTTGACATCAGAAAACAAGACGAGAATACAGAGGGT	1848
1849	GATCTGGAGTCTCTTCAATTAACATTTATGGTGTCTTTGACGGACATGGCGGTT	1903



9/13

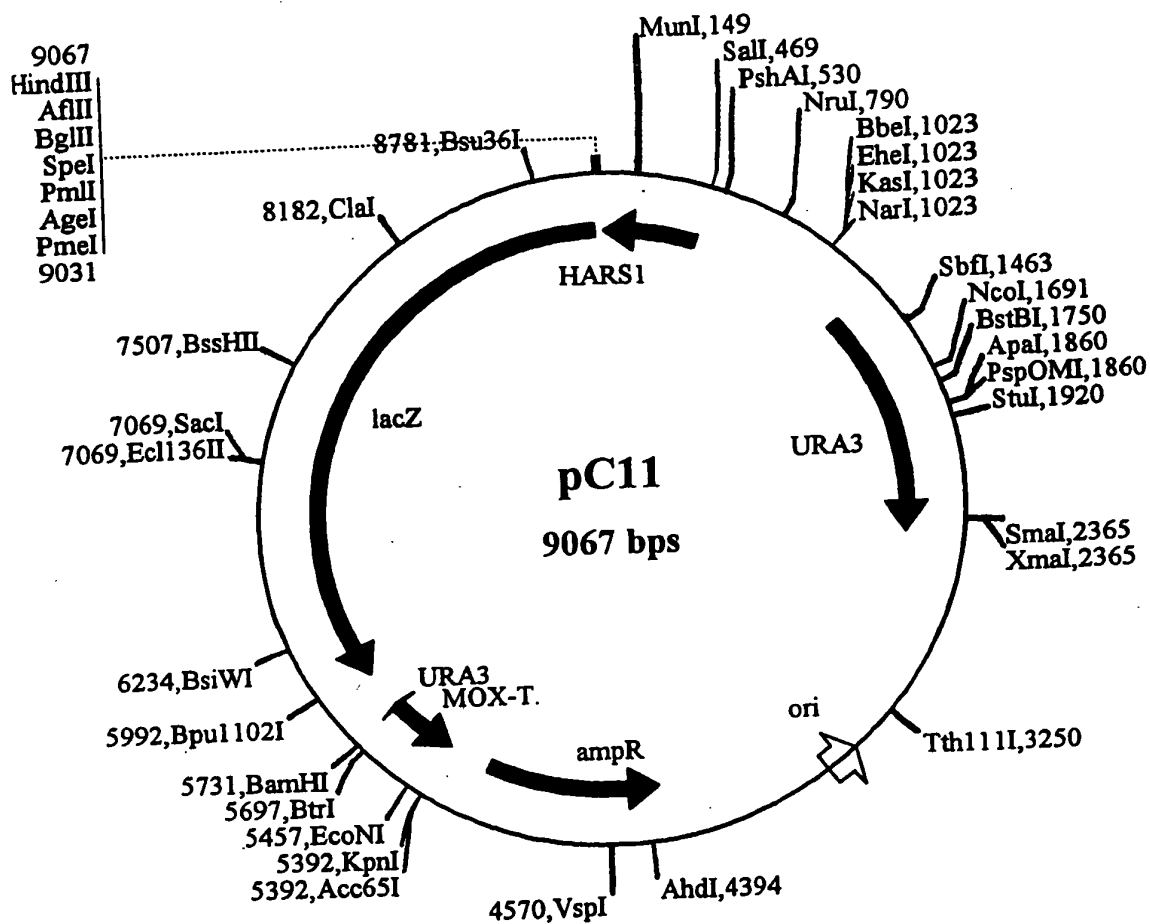


FIGURE 7



10/13

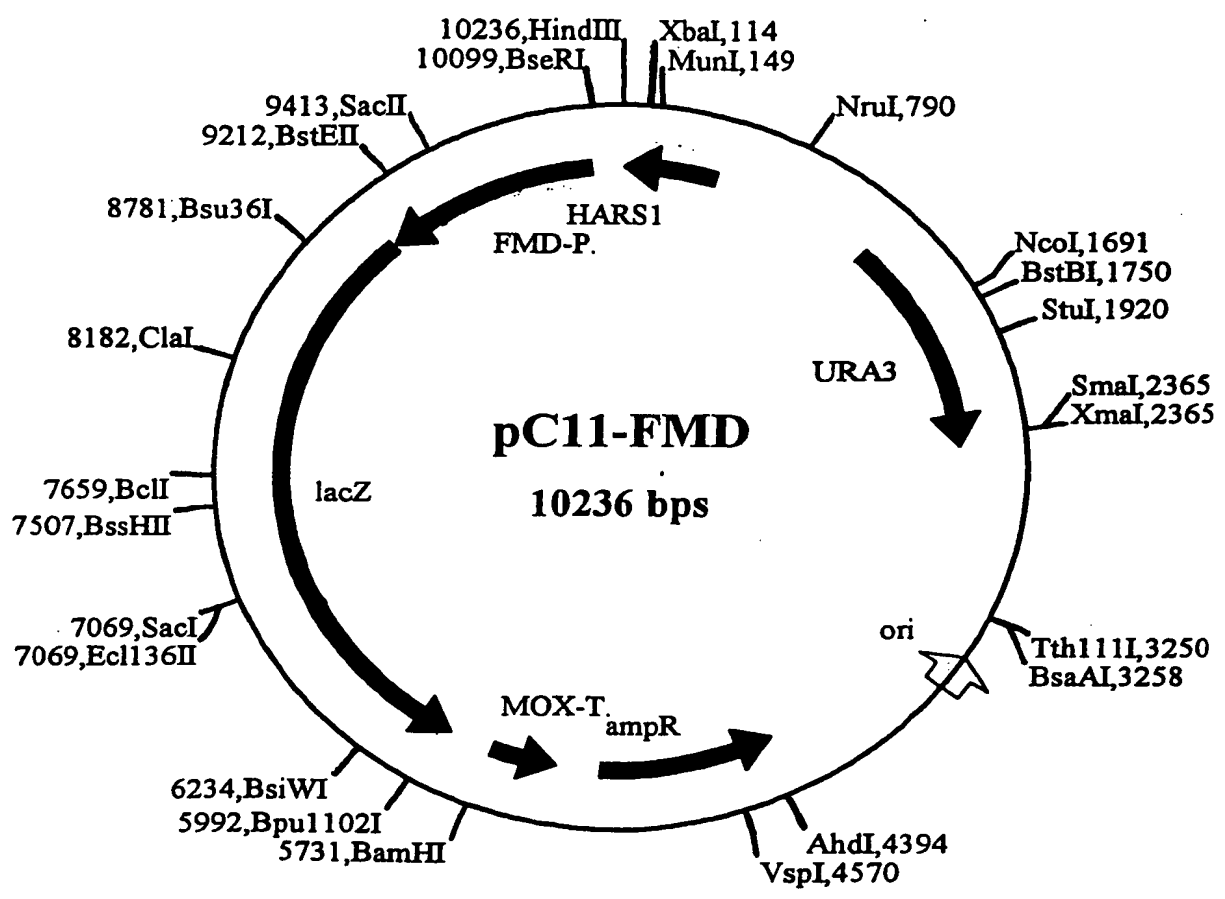


FIGURE 8

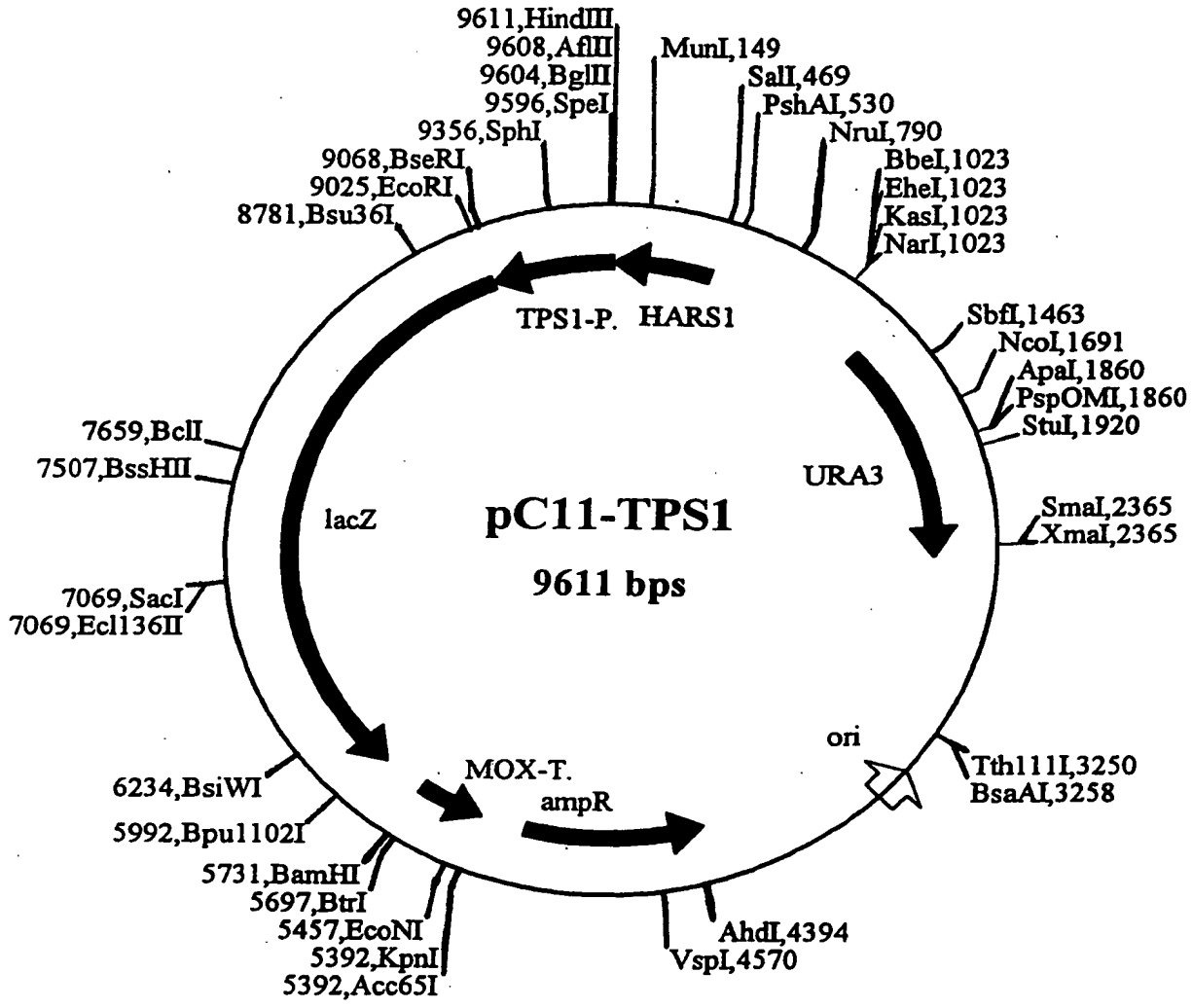


FIGURE 9



12/13

FIG. 10A

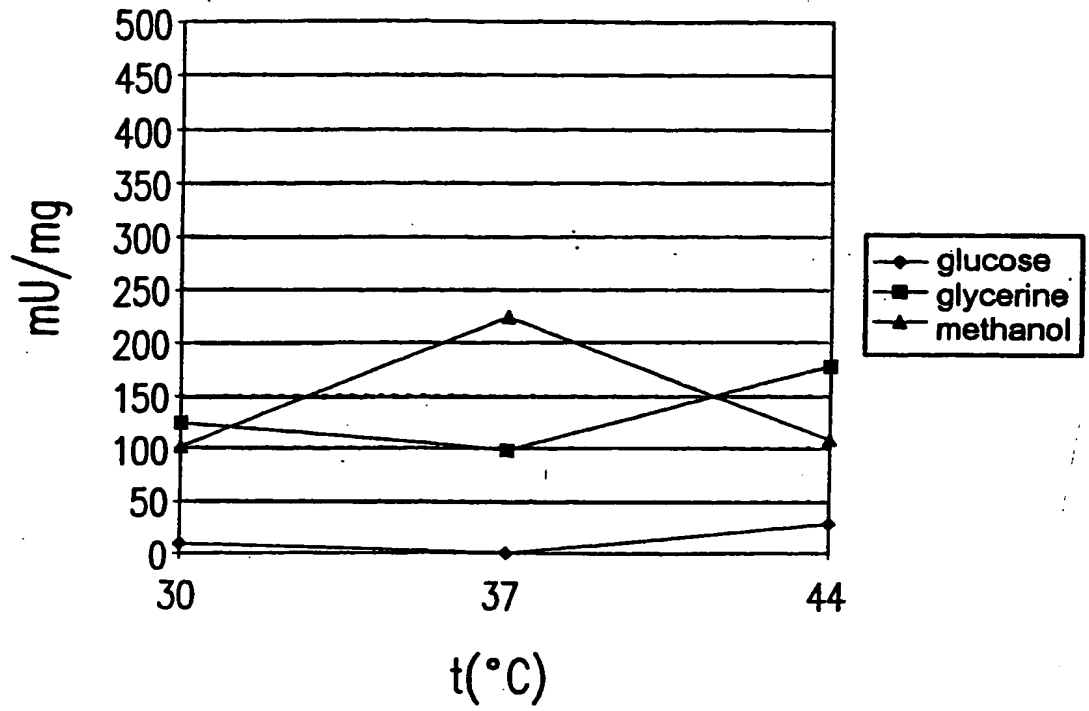
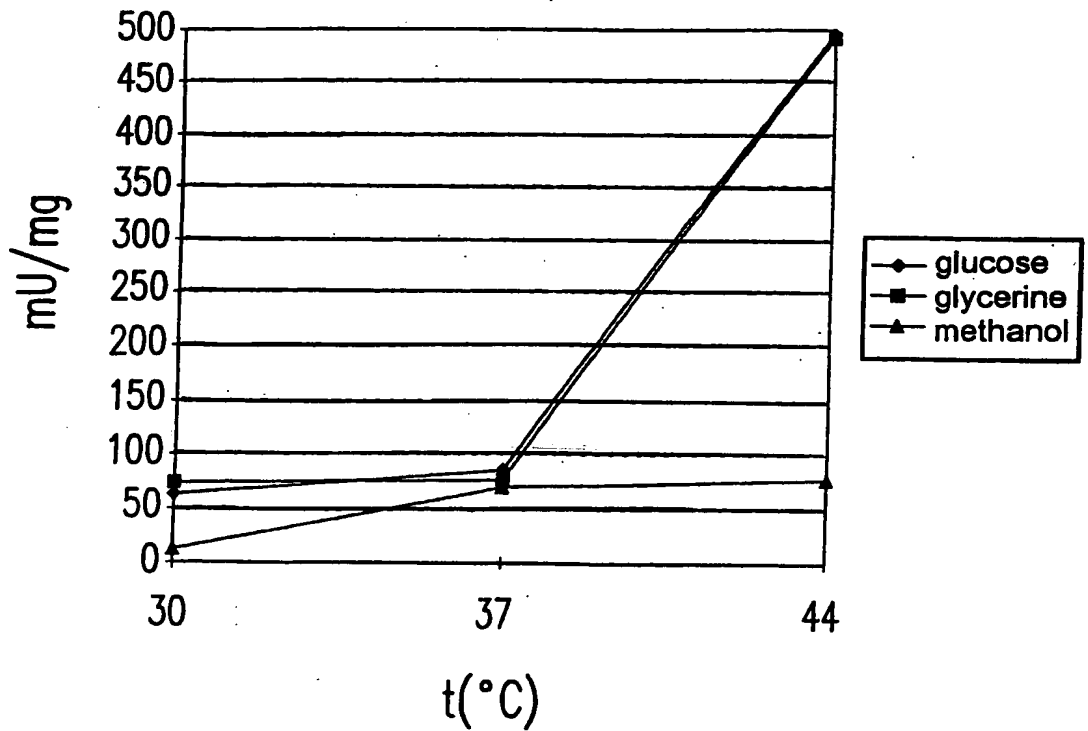


FIG. 10B





13/13

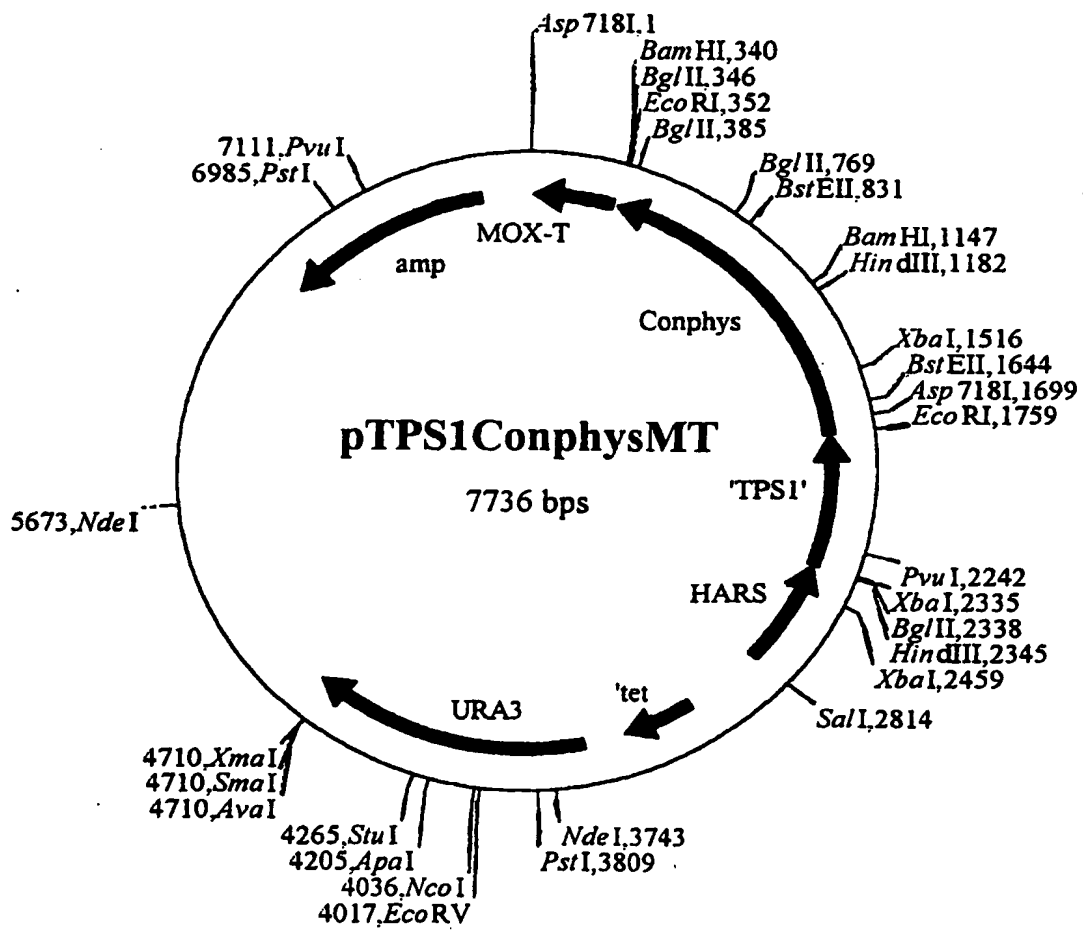


FIG. 11